

SEQUENCE LISTING

<110> Presnell, Scott R.
 Kuestner, Rolf E.
 Gao, Zeren

<120> Human Cytokine Receptor

<130> 00-49

<160> 13

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2383

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (86)...(2344)

<400> 1

ccgcccgcggc	caccggccac	tcggggctgg	ccagcgccgg	gcggccgggg	cgcagagaac	60
ggcctggctg	ggcgagcgca	cggcc	atg	gcc	ccg	61
			Met	Ala	Pro	Trp
			Leu	Gln	Leu	Cys
						Ser
			1		5	

gtc	ttc	ttt	acg	gtc	aac	gcc	tgc	ctc	aac	ggc	tcg	cag	ctg	gct	gtg	160
Val	Phe	Phe	Thr	Val	Asn	Ala	Cys	Leu	Asn	Gly	Ser	Gln	Leu	Ala	Val	
10															25	

gcc	gct	ggc	ggg	tcc	ggc	cgc	gcg	ggc	gcc	gac	acc	tgt	ggc	tgg	208
Ala	Ala	Gly	Gly	Ser	Gly	Arg	Ala	Arg	Gly	Ala	Asp	Thr	Cys	Gly	Trp
30															40

agg	atg	aaa	gct	gcc	cga	ccc	cg	ttt	tgt	gtt	gct	aat	gag	gga	256
Arg	Met	Lys	Ala	Ala	Ala	Arg	Pro	Arg	Leu	Cys	Val	Ala	Asn	Glu	Gly
45															55

gtg	ggg	cca	gcc	agc	aga	aac	agt	ggg	ctg	tac	aac	atc	acc	ttc	aaa	304
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys			
60	65	70	
tat gac aat tgt acc acc tac ttg aat cca gtg ggg aag cat gtg att			352
Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile			
75	80	85	
gct gac gcc cag aat atc acc atc agc cag tat gct tgc cat gac caa			400
Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln			
90	95	100	105
gtg gca gtc acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa ttc			448
Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe			
110	115	120	
ctg aaa gga ttt cgg gta ata ctg gag gag ctg aag tcg gag gga aga			496
Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg			
125	130	135	
cag tgc caa caa ctg att cta aag gat ccg aag cag ctc aac agt agc			544
Gln Cys Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser			
140	145	150	
ttc aaa aga act gga atg gaa tct caa cct ttc ctg aat atg aaa ttt			592
Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe			
155	160	165	
gaa acg gat tat ttc gta aag gtt gtc cct ttt cct tcc att aaa aac			640
Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile Lys Asn			
170	175	180	185
gaa acg aat tac cac cct ttc ttt aga acc cga gcc tgt gac ctg			688
Glu Ser Asn Tyr His Pro Phe Phe Arg Thr Arg Ala Cys Asp Leu			
190	195	200	
ttg tta cag ccg gac aat cta gct tgt aaa ccc ttc tgg aag cct cgg			736
Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg			
205	210	215	
aac ctg aac atc agc cag cat ggc tcg gac atg cag gtg tcc ttc gac			784
Asn Leu Asn Ile Ser Gln His Gly Ser Asp Asp Met Gln Val Ser Phe Asp			
220	225	230	

cat gca ccg cac aac ttc ggc ttc cgt ttc tat ctt cac tac aag His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys 235 240 245	832
ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag gag caa Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln 250 255 260 265	880
act aca gag acg acc agc tgc ctc ctt caa aat gtt tct cca ggg gat Thr Thr Glu Thr Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp 270 275 280	928
tat ata att gag ctg gtg gat gac act aac aca aca aga aaa gtg atg Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met 285 290 295	976
cat tat gcc tta aag cca gtg cac tcc ccg tgg gcc ggg ccc atc aga His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg 300 305 310	1024
gcc gtg gcc atc aca gtg cca ctg gta gtc ata tcg gca ttc gcg acg Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr 315 320 325	1072
ctc ttc act gtg atg tgc cgc aag aag caa caa gaa aat ata tat tca Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser 330 335 340 345	1120
cat tta gat gaa gag agc tct gag tct tcc aca tac act gca gca ctc His Leu Asp Glu Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu 350 355 360	1168
cca aga gag agg ctc cgg ccg cgg aag gtc ttt ctc tgc tat tcc Pro Arg Glu Arg Leu Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser 365 370 375	1216
agt aaa gat ggc cag aat cac atg aat gtc gtc cag tgt ttc gcc tac Ser Lys Asp Gly Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr 380 385 390	1264
ttc ctc cag gac ttc tgt ggc tgt gag gtg gct ctg gac ctg tgg gaa Phe Leu Gln Asp Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu 395 400 405	1312

gac ttc agc ctc tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys 410 415 420 425	1360
atc cac gag tcc cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys 430 435 440	1408
tac ttt gtg gac aag aag aac tac aaa cac aaa gga ggt ggc cga ggc Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Arg Gly 445 450 455	1456
tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu 460 465 470	1504
aag ctc cgc cag gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt Lys Leu Arg Gln Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe 475 480 485	1552
atc gcc gtc tac ttt gat tat tcc tgc gag gga gac gtc ccc ggt atc Ile Ala Val Tyr Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile 490 495 500 505	1600
cta gac ctg agt acc aag tac aga ctc atg gac aat ctt cct cag ctc Leu Asp Leu Ser Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu 510 515 520	1648
tgt tcc cac ttg cac tcc cga gac cac ggc ctc cag gag ccg ggg cag Cys Ser His Leu His Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln 525 530 535	1696
cac acg cga cag ggc agc aga agg aac tac ttc cgg agc aag tca ggc His Thr Arg Gln Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly 540 545 550	1744
cggttcccta tac gtc gcc att tgc aac atg cac cag gag ttt att gac gag Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu 555 560 565	1792
gag ccc gac tgg ttc gaa aag cag ttc gtt ccc ttc cat cct cct cca	1840

Glu	Pro	Asp	Trp	Phe	Glu	Lys	Gln	Phe	Val	Pro	Phe	His	Pro	Pro	Pro
570				575				580				585			
ctg	cgc	tac	cg	gag	cca	gtc	ttg	gag	aaa	ttt	gat	tcg	ggc	ttg	gtt
Leu	Arg	Tyr	Arg	Glu	Pro	Val	Leu	Glu	Lys	Phe	Asp	Ser	Gly	Leu	Val
							590			595			600		
tta	aat	gat	gtc	atg	tgc	aaa	cca	ggg	cct	gag	agt	gac	ttc	tgc	cta
Leu	Asn	Asp	Val	Met	Cys	Lys	Pro	Gly	Pro	Glu	Ser	Asp	Phe	Cys	Leu
							605			610			615		
aag	gta	gag	g	cg	g	ct	tt	gg	g	ca	cc	g	cc	tcc	cag
Lys	Val	Glu	Ala	Ala	Val	Leu	Gly	Ala	Thr	Gly	Pro	Ala	Asp	Ser	Gln
			620				625					630			
cac	gag	agt	cag	cat	ggg	ggc	ctg	gac	caa	gac	ggg	gag	ggc	cgg	cct
His	Glu	Ser	Gln	His	Gly	Gly	Leu	Asp	Gln	Asp	Gly	Glu	Ala	Arg	Pro
			635				640					645			
gcc	ctt	gac	gg	t	agc	g	cc	ctg	caa	ccc	ctg	ctg	cac	acg	gtg
Ala	Leu	Asp	Gly	Ser	Ala	Ala	Leu	Gln	Pro	Leu	Leu	His	Thr	Val	Lys
			650				655			660			665		
gcc	ggc	agc	ccc	tcg	gac	atg	ccg	cg	gac	tca	ggc	atc	tat	gac	tcg
Ala	Gly	Ser	Pro	Ser	Asp	Met	Pro	Arg	Asp	Ser	Gly	Ile	Tyr	Asp	Ser
			670				675					680			
tct	gtg	ccc	tca	tcc	gag	ctg	tct	ctg	cca	ctg	atg	gaa	gg	ctc	tcg
Ser	Val	Pro	Ser	Ser	Glu	Leu	Ser	Leu	Pro	Leu	Met	Glu	Gly	Leu	Ser
			685				690					695			
acg	gac	cag	aca	gaa	acg	tct	tcc	ctg	acg	gag	acg	gtg	tcc	tcc	tct
Thr	Asp	Gln	Thr	Glu	Thr	Ser	Ser	Leu	Thr	Glu	Ser	Val	Ser	Ser	Ser
			700				705					710			
tca	ggc	ctg	gg	t	ag	g	gg	gaa	cct	cct	ggc	ctt	cct	tcc	aag
Ser	Gly	Leu	Gly	Glu	Glu	Pro	Pro	Ala	Leu	Pro	Ser	Lys	Leu	Leu	
			715				720					725			
tct	tct	ggg	tca	tgc	aaa	gca	gat	ctt	gg	tgc	cgc	agc	tac	act	gat
Ser	Ser	Gly	Ser	Cys	Lys	Ala	Asp	Leu	Gly	Cys	Arg	Ser	Tyr	Thr	Asp
			730				735					740			745

gaa ctc cac gcg gtc gcc cct ttg taacaaaacg aaagagtcta agcattgcca 2374
 Glu Leu His Ala Val Ala Pro Leu
 750

cttttagctg 2383

<210> 2
 <211> 753
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val Asn Ala
 1 5 10 15
 Cys Leu Asn Gly Ser Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg
 20 25 30
 Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Met Lys Ala Ala Ala Arg
 35 40 45
 Pro Arg Leu Cys Val Ala Asn Glu Gly Val Gly Pro Ala Ser Arg Asn
 50 55 60
 Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr Thr Tyr
 65 70 75 80
 Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn Ile Thr
 85 90 95
 Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp
 100 105 110
 Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile
 115 120 125
 Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu
 130 135 140
 Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly Met Glu
 145 150 155 160
 Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys
 165 170 175
 Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe
 180 185 190
 Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu
 195 200 205
 Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His
 210 215 220
 Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe Gly
 225 230 235 240

Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro Phe
 245 250 255
 Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Thr Thr Ser Cys
 260 265 270
 Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp
 275 280 285
 Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro Val
 290 295 300
 His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro
 305 310 315 320
 Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys Arg
 325 330 335
 Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Ser
 340 345 350
 Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg Pro
 355 360 365
 Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn His
 370 375 380
 Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys Gly
 385 390 395 400
 Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu
 405 410 415
 Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe Ile
 420 425 430
 Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn
 435 440 445
 Tyr Lys His Lys Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu Phe
 450 455 460
 Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys Gln
 465 470 475 480
 Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp Tyr
 485 490 495
 Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys Tyr
 500 505 510
 Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser Arg
 515 520 525
 Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser Arg
 530 535 540
 Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala Ile
 545 550 555 560
 Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu Lys
 565 570 575

Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro Val
 580 585 590
 Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met Cys Lys
 595 600 605
 Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val Leu
 610 615 620
 Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly Gly
 625 630 635 640
 Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser Ala Ala
 645 650 655
 Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp Met
 660 665 670
 Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu
 675 680 685
 Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr Ser
 690 695 700
 Ser Leu Thr Glu Ser Val Ser Ser Ser Gly Leu Gly Glu Glu Glu
 705 710 715 720
 Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys Ala
 725 730 735
 Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val Ala Pro
 740 745 750
 Leu

<210> 3

<211> 2259

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the
amino acid sequence of SEQ ID NO:2.

<221> misc_feature

<222> (1)...(2259)

<223> n = A,T,C or G

<400> 3

atggcnccnt	ggytncaryt	ntgywsngtn	ttyttyacng	tnaaygcntg	yytnaaayggn	60
wsncarytng	cngtngcngc	nggnggnwsn	ggngmngncm	gngngncng	ya	120
tggmgnatga	argcngcngc	nmgnccnmgn	ytntgygtng	cnaaygargg	ngtnggnccn	180
gcnwsnmgna	aywsngngnyt	ntayaayath	acnttyaart	aygayaayt	ycnacnctay	240

ytnaayccng	tnggnaarca	ygtathgcn	gaygcncara	ayathacnat	hwsncartay	300
gcntgycayg	aycargtngc	ngtnacnath	ytntgwsnc	cnggncnyt	nggnathgar	360
ttyytnaarg	gnttymngt	nathyngar	garytnaarw	sngarggnmg	ncartgycar	420
carytnathy	tnaargaycc	naarcarytn	aaywsnwsnt	tyaarmgnac	nggnatggar	480
wsncarcnt	tyttnaayat	gaarttgar	acngaytayt	tygtnaargt	ngtnccntty	540
ccnwsnatha	araaygarws	naaytaycay	ccnttptyt	tygnacnmg	ngcntggyay	600
ytnytnytc	arcengayaa	yytngcntgy	aarcnttvt	ggaarccnmg	naayttnaay	660
athwsncarc	ayggnwsnga	yatgcargtn	wsnttygyc	aygcncnc	yaayttyggn	720
ttymgntyt	tytayttnca	ytayaarytn	aarcaygarg	gnccnityaa	rmgnaaracn	780
tgyaarcarg	arcaracnac	ngaracnacn	wsntgyttny	tncaraaygt	wsncncngn	840
gaytayatha	thgarytngt	ngaygayaacn	aayacnacnm	gnaargtnat	gcaytaygn	900
ytnaarcng	tncaywsncc	ntggcngn	cnathmng	cngtngcnat	hacngtnccn	960
ytngtngtna	thwsngcntt	ygcnacnyt	ttyacngtna	tgtgymgnna	raarcarcar	1020
garaayathht	aywsncayyt	ngaygargar	wsnwsngarw	snwsnacnta	yacngengcn	1080
ytnccnmng	armgnytmg	nccnmgnccn	aargtntt	tntgtytayws	nwsnaargay	1140
ggncaraaayc	ayatgaaygt	ngtncartgy	ttygcntayt	tytncarga	ytttytgyggn	1200
tgygargtng	cnytngayyt	ntgggargay	ttywsnytnt	gymgnargg	ncarmgnar	1260
tgggnathc	araarathca	yarwsncar	ttyathathg	tngtnityws	naarggnatg	1320
aartayttyg	tngayaaraa	raaytayaar	cayaarggng	gnngnmgng	wsnsgnaar	1380
ggngaryntt	tytngtngc	ngtnwsncn	athgcngara	arytnmgnca	rgcnaarcar	1440
wsnwsnwsng	cngcnytnws	naarttayth	gcngrntayt	tygatayws	ntgygarggn	1500
gaygtncng	gnathyngta	yytwnwsnacn	aartaymgn	tnatggyaa	yytncncar	1560
ytntgwsnc	aytncayws	rmngngaycay	ggnyticarg	arcnngnca	rcayacnmg	1620
carggnwsnm	gnmgnnaa	yttymgnwsn	aarwsnsgn	gnwsnytna	ygtngcnath	1680
tgyaayatgc	aycarattyat	hgaygargar	cngaytgg	tygaraarca	rtytgnccn	1740
ttycayccnc	cnccnytnmg	ntaymgnar	cngtngtng	aarattyga	ywsngnytn	1800
gtyntraayg	aygtnatgt	yaarcncngn	cngarwsng	ayttytgyt	naargtngar	1860
gcngcngtny	tnggngcnac	nggnccngcn	gaywsncarc	aygarwsnc	rcayggngn	1920
ytnngaycarg	ayggngargc	nmgnccngcn	ytnngaygnw	sngcngcnyt	ncarcnnyt	1980
ytnccayacng	tnaargcngg	wsnccnwsn	gayatgcnm	gngaywsng	nathtaygay	2040
wsnwsngtn	cnwsnwsng	rytnwsnyt	ccnytnatgg	arggnynws	nacngaycar	2100
acngaracnw	snwsnytnac	ngarwsngtn	wsnwsnwsnw	sngnytngg	ngargargar	2160
ccnccngn	tnccnwsnna	rytnytnwsn	wsnggnwsnt	gyaargcnga	yytngngtgy	2220
mgnwsntaya	cngaygaryl	ncaygcngtn	gcncnnyt			2259

<210> 4

<211> 2383

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (86)....(2344)

<400> 4			
ccgcccggc caccggccac tcggggctgg ccaggcgccg gccccgggg cgagagaac ggcctggctg ggcgagcga cggcc atg gcc ccg tgg ctg cag ctc tgc tcc Met Ala Pro Trp Leu Gln Leu Cys Ser	60 112		
1 5			
gtc ttc ttt acg gtc aac gcc tgc ctc aac ggc tcg cag ctg gct gtg Val Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Val	160		
10 15 20 25			
gcc gct ggc ggg tcc ggc cgc gcg cgg ggc gcc gac acc tgt ggc tgg Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp Thr Cys Gly Trp	208		
30 35 40			
agg atg aaa gcg gct gcc cga ccc cgg ctt tgt gtt gct aat gag gga Arg Met Lys Ala Ala Arg Pro Arg Leu Cys Val Ala Asn Glu Gly	256		
45 50 55			
gtg ggg cca gcc agc aga aac agt ggg ctg tac aac atc acc ttc aaa Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys	304		
60 65 70			
tat gac aat tgt acc acc tac ttg aat cca gtg ggg aag cat gtg att Tyr Asp Asn Cys Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile	352		
75 80 85			
gtc gac gcc cag aat atc acc atc agc cag tat gct tgc cat gac caa Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln	400		
90 95 100 105			
gtg gca gtc acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa ttc Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe	448		
110 115 120			
ctg aaa gga ttt cgg gta ata ctg gag gag ctg aag tcg gag gga aga Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg	496		
125 130 135			
cag tgc caa caa ctg att cta aag gat ccg aag cag ctc aac agt agc Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser	544		
140 145 150			

ttc aaa aga act gga atg gaa tct caa cct ttc ctg aat atg aaa ttt Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe 155 160 165	592
gaa acg gat tat ttc gta aag gtt gtc cct ttt cct tcc att aaa aac Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile Lys Asn 170 175 180 185	640
gaa agc aat tac cac cct ttc ttt aga acc cga gcc tgt gac ctg Glu Ser Asn Tyr His Pro Phe Phe Arg Thr Arg Ala Cys Asp Leu 190 195 200	688
ttg tta cag ccg gac aat cta gct tgt aaa ccc ttc tgg aag cct ccg Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg 205 210 215	736
aac ctg aac atc agc cag cat ggc tcg gac atg cag gtg tcc ttc gac Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser Phe Asp 220 225 230	784
cac gca ccg cac aac ttc ggc ttc cgt ttc tat ctt cac tac aag His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys 235 240 245	832
ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag gag caa Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln 250 255 260 265	880
act aca gag atg acc agc tgc ctc ctt caa aat gtt tct cca ggg gat Thr Thr Glu Met Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp 270 275 280	928
tat ata att gag ctg gtg gat gac act aac aca aca aga aaa gtg atg Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met 285 290 295	976
cat tat gcc tta aag cca gtg cac tcc ccg tgg gcc ggg ccc atc aga His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg 300 305 310	1024
gcc gtg gcc atc aca gtg cca ctg gta gtc ata tcg gca ttc gcg acg Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr 315 320 325	1072

ctc ttc act gtg atg tgc cgc aag aag caa caa gaa aat ata tat tca Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser 330 335 340 345	1120
cat tta gat gaa gag agc tct gag tct tcc aca tac act gca gca ctc His Leu Asp Glu Glu Ser Ser Glu Ser Thr Tyr Thr Ala Ala Leu 350 355 360	1168
cca aga gag agg ctc cgg ccg ccg aag gtc ttt ctc tgc tat tcc Pro Arg Glu Arg Leu Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser 365 370 375	1216
agt aaa gat ggc cag aat cac atg aat gtc gtc cag tgt ttc gcc tac Ser Lys Asp Gly Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr 380 385 390	1264
ttc ctc cag gac ttc tgt ggc tgt gag gtg gct ctg gac ctg tgg gaa Phe Leu Gln Asp Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu 395 400 405	1312
gac ttc agc ctc tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys 410 415 420 425	1360
atc cac gag tcc cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys 430 435 440	1408
tac ttt gtg gac aag aag aac tac aaa cac aaa gga ggt ggc cga ggc Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Arg Gly 445 450 455	1456
tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu 460 465 470	1504
aag ctc cgc cag gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt Lys Leu Arg Gln Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe 475 480 485	1552
atc gcc gtc tac ttt gat tat tcc tgc gag gga gac gtc ccc ggt atc	1600

Ile Ala Val Tyr Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile			
490	495	500	505
cta gac ctg agt acc aag tac aga ctc atg gac aat ctt cct cag ctc			1648
Leu Asp Leu Ser Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu			
510	515	520	
tgt tcc cac ctg cac tcc cga gac cac ggc ctc cag gag ccg ggg cag			1696
Cys Ser His Leu His Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln			
525	530	535	
cac acg cga cag ggc agc aga agg aac tac ttc cgg agc aag tca ggc			1744
His Thr Arg Gln Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly			
540	545	550	
cgg tcc cta tac gtc gcc att tgc aac atg cac cag ttt att gac gag			1792
Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu			
555	560	565	
gag ccc gac tgg ttc gaa aag cag ttc gtt ccc ttc cat cct cct cca			1840
Glu Pro Asp Trp Phe Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro			
570	575	580	585
ctg cgc tac cgg gag cca gtc ttg gag aaa ttt gat tcg ggc ttg gtt			1888
Leu Arg Tyr Arg Glu Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val			
590	595	600	
tta aat gat gtc atg tgc aaa cca ggg cct gag agt gac ttc tgc cta			1936
Leu Asn Asp Val Met Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu			
605	610	615	
aag gta gag gcg gct gtt ctt ggg gca acc gga cca gcc gac tcc cag			1984
Lys Val Glu Ala Ala Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln			
620	625	630	
cac gag agt cag cat ggg ggc ctg gac caa gac ggg gag gcc cgcc cct			2032
His Glu Ser Gln His Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro			
635	640	645	
gcc ctt gac ggt agc gcc gcc ctg caa ccc ctg ctg cac acg gtg aaa			2080
Ala Leu Asp Gly Ser Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys			
650	655	660	665

gcc ggc agc ccc tcg gac atg ccg cg ^g gac tca ggc atc tat gac tcg Ala Gly Ser Pro Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser 670 675 680	2128
tct gtg ccc tca tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg Ser Val Pro Ser Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser 685 690 695	2176
acg gac cag aca gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct Thr Asp Gln Thr Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser 700 705 710	2224
tca ggc ctg ggt gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc Ser Gly Leu Gly Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu 715 720 725	2272
tct tct ggg tca tgc aaa gca gat ctt ggt tgc cgc agc tac act gat Ser Ser Gly Ser Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp 730 735 740 745	2320
gaa ctc cac gcg gcc ccc ttg taacaaaacg aaagagtcta agcattgcc Glu Leu His Ala Ala Ala Pro Leu 750	2374
cttttagctg	2383
<210> 5 <211> 753 <212> PRT <213> Homo sapiens	
<400> 5 Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val Asn Ala 1 5 10 15 Cys Leu Asn Gly Ser Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg 20 25 30 Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Met Lys Ala Ala Ala Arg 35 40 45 Pro Arg Leu Cys Val Ala Asn Glu Gly Val Gly Pro Ala Ser Arg Asn 50 55 60 Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr Thr Tyr 65 70 75 80	

Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn Ile Thr
 85 90 95
 Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp
 100 105 110
 Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile
 115 120 125
 Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu
 130 135 140
 Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly Met Glu
 145 150 155 160
 Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys
 165 170 175
 Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe
 180 185 190
 Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu
 195 200 205
 Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His
 210 215 220
 Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe Gly
 225 230 235 240
 Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro Phe
 245 250 255
 Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Met Thr Ser Cys
 260 265 270
 Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp
 275 280 285
 Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro Val
 290 295 300
 His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro
 305 310 315 320
 Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys Arg
 325 330 335
 Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Ser
 340 345 350
 Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg Pro
 355 360 365
 Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn His
 370 375 380
 Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys Gly
 385 390 395 400
 Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu
 405 410 415

Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe Ile
 420 425 430
 Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn
 435 440 445
 Tyr Lys His Lys Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu Phe
 450 455 460
 Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys Gln
 465 470 475 480
 Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp Tyr
 485 490 495
 Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys Tyr
 500 505 510
 Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser Arg
 515 520 525
 Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser Arg
 530 535 540
 Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala Ile
 545 550 555 560
 Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu Lys
 565 570 575
 Gln Phe Val Pro Phe His Pro Pro Leu Arg Tyr Arg Glu Pro Val
 580 585 590
 Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met Cys Lys
 595 600 605
 Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val Leu
 610 615 620
 Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly Gly
 625 630 635 640
 Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser Ala Ala
 645 650 655
 Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp Met
 660 665 670
 Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu
 675 680 685
 Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr Ser
 690 695 700
 Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu Glu
 705 710 715 720
 Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys Ala
 725 730 735
 Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Ala Ala Pro
 740 745 750

Leu

<210> 6
 <211> 2259
 <212> DNA
 <213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:5.

<221> misc_feature
 <222> (1)...(2259)
 <223> n = A,T,C or G

<400> 6

atggcncnt ggytnccaryt ntgywsngtn ttyttyacng tnaaygcntg yytnaaygg	60
wsncarytng cngtngcngc nggnggnwsn ggnmgngcnm gnggngcnga yacntgygg	120
tggmgnatg argcngcngc nmgnccnmgn ynttgygtng cnaaygargg ntgnngccn	180
gcnwsnmgna aywsngnyt ntayaayath acnntyart ayygayaaytg yacnacntay	240
ytnaayccng tnggnaarca ygttnathgcn gaygcncara ayathacnat hwsncartay	300
gcntgycayg aycargtngc ngtnacnath ytnntggwsnc cnggngcnyt nggnathgar	360
ttyytnaarg gnttymgnnt nathytngar ygttnaargw sngargng ncartygcar	420
carytnathy thaargaycc naarcarytn aaywsnwsnt tyaarmgnac nggnatggar	480
wsncarcntt tyytnaayat gaarttygar acngaytayt tyytnaargt ntncntty	540
ccnwsnathaa aaraygarws naaytaycay ccnttymgn tymgnacnmg ncntgyg	600
ytnytnytncc arccngayaa ytnccntgy aarccntt ytnccntt ggaarcnmg naaytynaay	660
athwsncarc ayygnwsnga yatgcargtn wsnttgyayc aygcncnca yaaytgygn	720
ttymgnntt tytaytnca ytnaayytn aarcaygarg ncncnttya rmgnaraacn	780
tgyaarcarg arcaracnac ngaratgacn wsntggytyn tncaraaygt nwsncnngn	840
gaytayatha thgatytngt ngaygayacn aayacnacnm gnaargtnat gcaytaygc	900
ytnaarcng tncaywsncc ntggcnggn ccnathmgng cngtngcnat hacngtncn	960
ytnngtngtna thwsngcnntt ygcncnctn ttnyacngtna tngtgygnna raarcarcar	1020
garaaytht aywsncayyt ngaygargar wsnwsnrgar snwsnacnta yacngcngn	1080
ytnccnmngn armgnytnmg nccnmgnccn aargtntt ytnytnytn tntgytawys nwsnaargay	1140
ggncaraayc ayatgaaygt ntgnccntgy ttnyacngtna ttnyacngtna ytttgygg	1200
tgygargtng cnytngayt ntgggargay ttnyacngtna ttnyacngtna ytttgygg	1260
tgggtngtngtna thwsngcnntt ygcncnctn ttnyacngtna tngtgygnna raarcarcar	1320
aartaytngtngtna thwsngcnntt ygcncnctn ttnyacngtna tngtgygnna raarcarcar	1380
gngcaraayc ayatgaaygt ntgnccntgy ttnyacngtna ttnyacngtna ytttgygg	1440
gngcaraayc ayatgaaygt ntgnccntgy ttnyacngtna ttnyacngtna ytttgygg	1500
gngcaraayc ayatgaaygt ntgnccntgy ttnyacngtna ttnyacngtna ytttgygg	1560
gngcaraayc ayatgaaygt ntgnccntgy ttnyacngtna ttnyacngtna ytttgygg	1620

carggnwsnm gnmgnaayta yttymgnwsn aarwsnggnm gnwsnynta ygtngcnath
 tgyaayatgc aycarttyat hgaygargar ccngaytggt tygaraarcia rtttygtncn
 ttycayccnc cnccnytnmg ntaymgnar ccngtnytna araarttyga ywsnggnytn
 gtnytnaayg aygtnatgt yaarcnngn ccngarwsng aytttygyt naargtngar
 gncngcnth tngngcnac ngnccnngn gaywsncarc aygarwsnca rcayggngn
 ytngaycarg ayggngarc nmgncnngn ytngaygnw sngcngcnth ncarcnthy
 ytnccayacng tnaargcngg nwsnccnwsn gayatgcnm gngaywsngg nathtaygay
 wswnwsngtnc cnwsnwsnra rytnwsnytn ccnytnatgg arggnytnws nacngaycar
 acngaracnw snwsnytnac ngarwsngtn wswnwsnsw snngnytnng ngargargar
 ccnccngcnth tnccnwsnaa rytnytnwsn wsngnwsnt gyaargcnga yytngngntg
 mgnwsntaya cngaygaryl ncaygcnac gcncnhyt

<210> 7
 <211> 2341
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (86)...(2302)

<400> 7

ccgcccgcggc caccgccccac tcggggctgg ccagcggcgg gcggccgggg cgcagagaac
 ggcctggctg ggcgagcgc a cggcc atg gcc cgg tgg ctg cag ctc tgc tcc
 Met Ala Pro Trp Leu Gln Leu Cys Ser
 1 5

60
112

gtc ttc ttt acg gtc aac gcc tgc ctc aac ggc tcg cag ctg gct gtg
 Val Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Val
 10 15 20 25

160

gcc gct ggc ggg tcc ggc cgc gcg cgg ggc gcc gac acc tgt ggc tgg
 Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp Thr Cys Gly Trp
 30 35 40

208

agg gga gtg ggg cca gcc agc aga aac agt ggg ctg tac aac atc acc
 Arg Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr
 45 50 55

256

ttc aaa tat gac aat tgt acc acc tac ttg aat cca gtg ggg aag cat
 Phe Lys Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His
 60 65 70

304

gtg att gct gac gcc cag aat atc acc atc agc cag tat gct tgc cat		352	
Val Ile Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His			
75	80	85	
gac caa gtg gca gtc acc att ctt tgg tcc cca ggg gcc ctc ggc atc		400	
Asp Gln Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile			
90	95	100	105
gaa ttc ctg aaa gga ttt cgg gta ata ctg gag gag ctg aag tcg gag		448	
Glu Phe Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu			
110	115	120	
gga aga cag tgc caa caa ctg att cta aag gat ccg aag cag ctc aac		496	
Gly Arg Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn			
125	130	135	
agt agc ttc aaa aga act gga atg gaa tct caa cct ttc ctg aat atg		544	
Ser Ser Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met			
140	145	150	
aaa ttt gaa acg gat tat ttc gta aag gtt gtc cct ttt cct tcc att		592	
Lys Phe Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile			
155	160	165	
aaa aac gaa agc aat tac cac cct ttc ttc ttt aga acc cga gcc tgt		640	
Lys Asn Glu Ser Asn Tyr His Pro Phe Phe Arg Thr Arg Ala Cys			
170	175	180	185
gac ctg ttg tta cag ccg gac aat cta gct tgt aaa ccc ttc tgg aag		688	
Asp Leu Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys			
190	195	200	
cct ccg aac ctg aac atc agc cag cat ggc tcg gac atg cag gtg tcc		736	
Pro Arg Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser			
205	210	215	
ttc gac cat gca ccg cac aac ttc ggc ttc cgt ttc tat ctt cac		784	
Phe Asp His Ala Pro His Asn Phe Gly Phe Arg Phe Tyr Leu His			
220	225	230	
tac aag ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag		832	
Tyr Lys Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln			
235	240	245	

gag caa act aca gag acg acc agc tgc ctc ctt caa aat gtt tct cca Glu Gln Thr Thr Glu Thr Thr Ser Cys Leu Leu Gln Asn Val Ser Pro 250 255 260 265	880
ggg gat tat ata att gag ctg gtg gat gac act aac aca aca aga aaa Gly Asp Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys 270 275 280	928
gtg atg cat tat gcc tta aag cca gtg cac tcc ccg tgg gcc ggg ccc Val Met His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro 285 290 295	976
atc aga gcc gtg gcc atc aca gtg cca ctg gta gtc ata tcg gca ttc Ile Arg Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe 300 305 310	1024
gcg acg ctc ttc act gtg atg tgc cgc aag caa caa gaa aat ata Ala Thr Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile 315 320 325	1072
tat tca cat tta gat gaa gag agc tct gag tct tcc aca tac act gca Tyr Ser His Leu Asp Glu Glu Ser Ser Glu Ser Thr Tyr Thr Ala 330 335 340 345	1120
gca ctc cca aga gag agg ctc cgg ccg ccg aag gtc ttt ctc tgc Ala Leu Pro Arg Glu Arg Leu Arg Pro Arg Pro Lys Val Phe Leu Cys 350 355 360	1168
tat tcc agt aaa gat ggc cag aat cac atg aat gtc gtc cag tgt ttc Tyr Ser Ser Lys Asp Gly Gln Asn His Met Asn Val Val Gln Cys Phe 365 370 375	1216
gcc tac ttc ctc cag gac ttc tgt ggc tgt gag gtg gct ctg gac ctg Ala Tyr Phe Leu Gln Asp Phe Cys Gly Cys Glu Val Ala Leu Asp Leu 380 385 390	1264
tgg gaa gac ttc agc ctc tgt aga gaa ggg cag aga gaa tgg gtc atc Trp Glu Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile 395 400 405	1312
cag aag atc cac gag tcc cag ttc atc att gtg gtt tgt tcc aaa ggt	1360

Gln Lys Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly				
410	415	420	425	
atg aag tac ttt gtg gac aag aac tac aaa cac aaa gga ggt ggc				1408
Met Lys Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly				
430	435	440		
cga ggc tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att				1456
Arg Gly Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile				
445	450	455		
gcc gaa aag ctc cgc cag gcc aag cag agt tcg tcc gcg gcg ctc agc				1504
Ala Glu Lys Leu Arg Gln Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser				
460	465	470		
aag ttt atc gcc gtc tac ttt gat tat tcc tgc gag gga gac gtc ccc				1552
Lys Phe Ile Ala Val Tyr Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro				
475	480	485		
ggc atc cta gac ctg agt acc aag tac aga ctc atg gac aat ctt cct				1600
Gly Ile Leu Asp Leu Ser Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro				
490	495	500	505	
cag ctc tgt tcc cac ttg cac tcc cga gac cac ggc ctc cag gag ccg				1648
Gln Leu Cys Ser His Leu His Ser Arg Asp His Gly Leu Gln Glu Pro				
510	515	520		
ggg cag cac acg cga cag ggc agc aga agg aac tac ttc cgg agc aag				1696
Gly Gln His Thr Arg Gln Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys				
525	530	535		
tca ggc cgg tcc cta tac gtc gcc att tgc aac atg cac cag ttt att				1744
Ser Gly Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile				
540	545	550		
gac gag gag ccc gac tgg ttc gaa aag cag ttc gtt ccc ttc cat cct				1792
Asp Glu Glu Pro Asp Trp Phe Glu Lys Gln Phe Val Pro Phe His Pro				
555	560	565		
cct cca ctg cgc tac cgg gag cca gtc ttg gag aaa ttt gat tcg ggc				1840
Pro Pro Leu Arg Tyr Arg Glu Pro Val Leu Glu Lys Phe Asp Ser Gly				
570	575	580	585	

ttg gtt tta aat gat gtc atg tgc aaa cca ggg cct gag agt gac ttc Leu Val Leu Asn Asp Val Met Cys Lys Pro Gly Pro Glu Ser Asp Phe 590 595 600	1888
tgc cta aag gta gag gcg gct gtt ctt ggg gca acc gga cca gcc gac Cys Leu Lys Val Glu Ala Ala Val Leu Gly Ala Thr Gly Pro Ala Asp 605 610 615	1936
tcc cag cac gag agt cag cat ggg ggc ctg gac caa gac ggg gag gcc Ser Gln His Glu Ser Gln His Gly Gly Leu Asp Gln Asp Gly Glu Ala 620 625 630	1984
cg ^g cct gcc ctt gac ggt agc gcc gcc ctg caa ccc ctg ctg cac acg Arg Pro Ala Leu Asp Gly Ser Ala Ala Leu Gln Pro Leu Leu His Thr 635 640 645	2032
gtg aaa gcc ggc agc ccc tcg gac atg ccg ccg gac tca ggc atc tat Val Lys Ala Gly Ser Pro Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr 650 655 660 665	2080
gac tcg tct gtg ccc tca tcc gag ctg tct ctg cca ctg atg gaa gga Asp Ser Ser Val Pro Ser Ser Glu Leu Ser Leu Pro Leu Met Glu Gly 670 675 680	2128
ctc tcg acg gac cag aca gaa acg tct tcc ctg acg gag agc gtg tcc Leu Ser Thr Asp Gln Thr Glu Thr Ser Ser Leu Thr Glu Ser Val Ser 685 690 695	2176
tcc tct tca ggc ctg ggt gag gag gaa cct cct gcc ctt cct tcc aag Ser Ser Ser Gly Leu Gly Glu Glu Pro Pro Ala Leu Pro Ser Lys 700 705 710	2224
ctc ctc tct tct ggg tca tgc aaa gca gat ctt ggt tgc cgc agc tac Leu Leu Ser Ser Gly Ser Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr 715 720 725	2272
act gat gaa ctc cac gcg gtc gcc cct ttg taacaaaacg aaagagtctta Thr Asp Glu Leu His Ala Val Ala Pro Leu 730 735	2322
agcattgcca cttagctg	2341

<210> 8
 <211> 739
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val Asn Ala
 1 5 10 15
 Cys Leu Asn Gly Ser Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg
 20 25 30
 Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Gly Val Gly Pro Ala Ser
 35 40 45
 Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr
 50 55 60
 Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn
 65 70 75 80
 Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile
 85 90 95
 Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg
 100 105 110
 Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu
 115 120 125
 Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly
 130 135 140
 Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe
 145 150 155 160
 Val Lys Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His
 165 170 175
 Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp
 180 185 190
 Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser
 195 200 205
 Gln His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn
 210 215 220
 Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly
 225 230 235 240
 Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Thr
 245 250 255
 Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu
 260 265 270
 Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys
 275 280 285

Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr
 290 295 300
 Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met
 305 310 315 320
 Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu
 325 330 335
 Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu
 340 345 350
 Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln
 355 360 365
 Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe
 370 375 380
 Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys
 385 390 395 400
 Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln
 405 410 415
 Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys
 420 425 430
 Lys Asn Tyr Lys His Lys Gly Gly Arg Gly Ser Gly Lys Gly Glu
 435 440 445
 Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala
 450 455 460
 Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe
 465 470 475 480
 Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr
 485 490 495
 Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His
 500 505 510
 Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly
 515 520 525
 Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val
 530 535 540
 Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe
 545 550 555 560
 Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu
 565 570 575
 Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met
 580 585 590
 Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala
 595 600 605
 Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His
 610 615 620

Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser
 625 630 635 640
 Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser
 645 650 655
 Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser
 660 665 670
 Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu
 675 680 685
 Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Gly Leu Gly Glu
 690 695 700
 Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys
 705 710 715 720
 Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val
 725 730 735
 Ala Pro Leu

<210> 9

<211> 2217

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:8.

<221> misc_feature

<222> (1)...(2217)

<223> n = A,T,C or G

<400> 9

atggccncntt	ggtytcnaryt	ntgywsngtn	ttyttyacng	tnaaygcntg	yytnaaygg	60
wsncarytng	cngtngcngc	ngngggwns	ggngngcncm	gngngcnga	ycacntgygg	120
tggmgngng	tnngnccngc	nwsnmgnaay	wsngngnynt	ayaayathac	nttyaartay	180
gayaaytgya	cnacntayyt	naayccngtn	ggnaarcayg	tnathgcng	ygcncaraay	240
athacnathw	sncartaygc	ntgycaygay	cargtngcng	tnacnathyt	ntggwsnccn	300
ggngcnytng	gnathgartt	yytnaarggn	ttymgngtna	thytnrgarga	rytnaarwsn	360
garggnmgnc	artgycarca	rytnathyt	aargayccna	arcarytnaa	ywsnwsntty	420
aarmgnacng	gnatggars	ncarcntty	yttnaayatga	arttygarac	ngaytayt	480
gtnaargtng	tnccnttycc	nwsnatha	aaygarwsna	aytaycaycc	nttyt	540
mgnacnmgng	cntygyayat	nytntycar	ccngayaaay	tngcnygaa	rccnttytgg	600
aarcnmgna	ayytnaayat	hwsncarcay	ggnwsgnay	tgcargtnws	nttygacy	660
gcncncaya	aytgyggntt	ymgnntt	tayytnccayt	ayaarytnaa	rcaygarggn	720
ccnttyaarm	gnaaracntg	yaarcargar	caracnacng	aracnacnws	ntgyytny	780

caraaygtnw	snccngngna	ytayathath	garytngtng	aygayacnaa	ycnacnmgm	840
aargtnatgc	aytaygcnyt	naarcngtn	caywsncnt	ggcngngcc	nathmngncn	900
gtngcnatha	cngtnccnyt	ngtngtnath	wsngcnrttyg	cnacnytntt	yacngtnatg	960
tgymgnaara	arcarcarga	raayathtay	wsncaytyng	aygargarws	nwsngarwsn	1020
wsnacntaya	cngcngcnyt	nccnmgngar	mgnytrmgnc	cnmgncncna	rgtnttyyt	1080
tgytaywsnw	snaargaygg	ncaraaycay	atgaaytng	tncartgytt	ycnctaytty	1140
ytncargayt	tytgyggnt	ygargtngcn	ytngaytnt	gggargaytt	ywsnytntgy	1200
mngngargnc	armgngart	ggtnathcar	aarathcayg	arwsncartt	yathathgtn	1260
gtntgywsna	arggnatgaa	rtayttygt	gayaaraara	aytayaarca	yaargnggn	1320
ggnmgnggnw	snggnaaarg	ngarytntty	ytngtngcng	twnsngcnat	hgcngraraar	1380
ytnmgnrcarg	cnaarcarws	nwsnwsngcn	gcnytnwsna	arttyathgc	ngtntaytty	1440
gaytaywsnt	gygarggng	ygtnccnggn	athytrngayy	twnsnacnaa	rtaymnytn	1500
atggayaayy	tnccncaryt	ntgywsncay	ytncaywsnm	gngaycaygg	nytncargar	1560
ccnggncarc	ayachmgnca	rggnwsrmgn	mgnaaaytayt	tymgnwsnaa	rwsnggnmgn	1620
wsnytntayg	tngcnathtg	yaayatgcay	carttyathg	aygargarcc	ngaytggty	1680
garaarcart	tygtncnctt	ycayccncn	ccnytrmgnt	aymgnarcc	ngtntyngar	1740
aarttygaw	snggnytngt	nytnaaygay	gtnatgtgya	arccnggncc	ngarwsngay	1800
tttytgyytna	argtngargc	ngcngtyn	ggngcnacng	gnccngcnga	ywsncarcay	1860
garwsncarc	ayggngnyt	ngaycargay	ggngargcm	gnccngcnyt	ngaygnwsn	1920
gncngcnyc	arccnytnt	ncayacngtn	aargcnggnw	snccnwsngna	yatgcnmgn	1980
gaywsngna	tthtaygayws	nwsngtnccn	wsnwsngary	twnsnytnc	nytnatggar	2040
ggnytnwsna	cngaycarac	ngaracnwsn	wsnytnacng	arwsngtnws	nwsnwsnwsn	2100
ggnytnngng	argargarcc	nccngcnyn	ccnwsnaary	trytnwsnw	nggnwsntgy	2160
aargcngayy	tngngntgy	mngwsntayacn	gaygarytnc	aygcngtngc	nccnyn	2217

<210> 10

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker.

<400> 10

Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Ser
1			5			10			15			

<210> 11

<211> 2443

<212> DNA

<213> Mouse

<220>

<221> CDS			
<222> (101)...(2317)			
<400> 11			
ctcgccgcgc gccgctacca ccggccccc ctcggacta gagagcgagc tacaggcagc aacctagccg agaccggccc aactggcga gcgtacggcc atg gcc ccg tgg ctg Met Ala Pro Trp Leu	60	115	
1 5			
cag ctc tgc tcc ttc ttc act gtc aac gcc tgt ctc aac ggc tcg Gln Leu Cys Ser Phe Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser	163		
10 15 20			
cag ctg gca gtg gcc gcg ggc tcc ggc cgc gcg agg ggc gcg gac Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp	211		
25 30 35			
acc tgt ggc tgg agg gga gtg ggg ccg gcc agc agg aac agc gga ctg Thr Cys Gly Trp Arg Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu	259		
40 45 50			
cac aac atc acc ttc aga tac gac aac tgt acc acc tac ttg aat ccc His Asn Ile Thr Phe Arg Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro	307		
55 60 65			
ggc ggc ggg aag cat gcg att gct gat gct cag aac atc acc atc agc Gly Gly Gly Lys His Ala Ile Ala Asp Ala Gln Asn Ile Thr Ile Ser	355		
70 75 80 85			
cag tac gct tgc cac gac cag gtg gca gtc acc att ctt tgg tcc cca Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp Ser Pro	403		
90 95 100			
ggg gcc ctt ggc att gaa ttc cta aaa gga ttc cga gtc atc ctg gag Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile Leu Glu	451		
105 110 115			
gag ctg aag tcg gag ggc aga cag tgc caa cag ctg att cta aag gac Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu Lys Asp	499		
120 125 130			
ccc aaa cag ctc aac agc agc ttc aga agg act gga atg gaa tct cag	547		

Pro Lys Gln Leu Asn Ser Ser Phe Arg Arg Thr Gly Met Glu Ser Gln	135	140	145	
cct ttc ctg aat atg aaa ttt gag acg gat tac ttt gta aag att gtc				595
Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys Ile Val	150	155	160	165
cct ttc cct tcc att aaa aat gaa agc aat tac cat ccc ttc ttc ttc				643
Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe Phe	170	175	180	
aga aca cgg gcc tgt gac ctg ttg tta caa cct gac aac ttg gcc tgt				691
Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu Ala Cys	185	190	195	
aag cct ttc tgg aag cct cga aac ctg aat atc agc cag cat ggt tct				739
Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His Gly Ser	200	205	210	
gac atg cac gtg tcc ttc gac cat gcc ccg cag aac ttc ggc ttc cgt				787
Asp Met His Val Ser Phe Asp His Ala Pro Gln Asn Phe Gly Phe Arg	215	220	225	
ggc ttc cat gtt ctc tat aag ctc aag cac gaa ggc ccc ttc agg cgg				835
Gly Phe His Val Leu Tyr Lys Leu Lys His Glu Gly Pro Phe Arg Arg	230	235	240	245
agg act tgc agg cag gac cag aat aca gag aca acc agc tgc ctc				883
Arg Thr Cys Arg Gln Asp Gln Asn Thr Glu Thr Thr Ser Cys Leu Leu	250	255	260	
caa aac gtt tct cca ggg gac tat atc att gag ctg gtg gat gac agc				931
Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp Asp Ser	265	270	275	
aac acc acc agg aaa gct gct cag tat gtg gtg aag tca gtg cag tct				979
Asn Thr Thr Arg Lys Ala Ala Gln Tyr Val Val Lys Ser Val Gln Ser	280	285	290	
ccc tgg gct gga ccc atc aga gct gtg gcc atc act gtg cct ctg gtt				1027
Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro Leu Val	295	300	305	

gtc ata tct gct ttc gca acc ctg ttc act gtg atg tgc aga aag aag			1075
Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys Arg Lys Lys			
310	315	320	325
caa caa gaa aat ata tat tca cat tta gat gaa gaa agc ccg gag tcg			1123
Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Pro Glu Ser			
330	335	340	
tcc aca tac gct gct ctc ccc aga gac agg ctc cgg cct cag ccc			1171
Ser Thr Tyr Ala Ala Ala Leu Pro Arg Asp Arg Leu Arg Pro Gln Pro			
345	350	355	
aag gtc ttc ctc tgc tac tcc aat aaa gat ggc cag aat cac atg aac			1219
Lys Val Phe Leu Cys Tyr Ser Asn Lys Asp Gly Gln Asn His Met Asn			
360	365	370	
gtg gtc cag tgt ttc gcc tat ttc ctg caa gat ttc tgt ggc tgt gag			1267
Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys Gly Cys Glu			
375	380	385	
gtg gct ctg gac ttg tgg gaa gat ttc agc ctc tgc aga gag ggg cag			1315
Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu Gly Gln			
390	395	400	405
aga gaa ttg gcc att cag aag atc cac gag tcc cag ttc atc att gtc			1363
Arg Glu Trp Ala Ile Gln Lys Ile His Glu Ser Gln Phe Ile Ile Val			
410	415	420	
gtg tgc tcc aaa ggc atg aag tac ttt gta gat aag aag aac ttc aga			1411
Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn Phe Arg			
425	430	435	
cac aaa gga ggc agc cgc ggc gag gcg caa ggc gag ttc ttc ctg gtg			1459
His Lys Gly Gly Ser Arg Gly Glu Ala Gln Gly Glu Phe Phe Leu Val			
440	445	450	
gcc gtg gca gcc att gct gag aag ctc cgt cag gcc aag cag agc tca			1507
Ala Val Ala Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys Gln Ser Ser			
455	460	465	
tct gcc gca ctg cgc aag ttc atc gcc gtc tac ttc gat tat tcc tgt			1555

Ser Ala Ala Leu Arg Lys Phe Ile Ala Val Tyr Phe Asp Tyr Ser Cys			
470	475	480	485
gaa ggg gat gta ccc tgc agc ctg gac ctg agc acc aag tac aag ctc			1603
Glu Gly Asp Val Pro Cys Ser Leu Asp Leu Ser Thr Lys Tyr Lys Leu			
490	495	500	
atg gac cac ctt cct gag ctc tgt gcc cat ctg cac tca gga gag cag			1651
Met Asp His Leu Pro Glu Leu Cys Ala His Leu His Ser Gly Glu Gln			
505	510	515	
gag gtg ctg ggt cag cac cca ggc cac agc agc aga agg aac tac ttc			1699
Glu Val Leu Gly Gln His Pro Gly His Ser Ser Arg Arg Asn Tyr Phe			
520	525	530	
cgg agc aaa tcg ggc cgc tcc ctg tat gtt gcc att tgc aac atg cac			1747
Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His			
535	540	545	
cag ttt att gat gag gag cct gac tgg ttt gag aag cag ttt ata ccc			1795
Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu Lys Gln Phe Ile Pro			
550	555	560	565
ttc caa cat ccc cct gtg cgc tac cag gag cca gtc ctg gag aaa ttt			1843
Phe Gln His Pro Pro Val Arg Tyr Gln Glu Pro Val Leu Glu Lys Phe			
570	575	580	
gac tca ggc ttg gtt tta aat gat gtc ata agc aaa cca ggg cca gag			1891
Asp Ser Gly Leu Val Leu Asn Asp Val Ile Ser Lys Pro Gly Pro Glu			
585	590	595	
agt gac ttc tgt cgg aaa gtc gag gct tgt gta ctt ggg gcc gct ggg			1939
Ser Asp Phe Cys Arg Lys Val Glu Ala Cys Val Leu Gly Ala Ala Gly			
600	605	610	
cca gcc gac tct tat tca tac ctg gag agt cag cat gta ggc ctg gac			1987
Pro Ala Asp Ser Tyr Ser Tyr Leu Glu Ser Gln His Val Gly Leu Asp			
615	620	625	
caa gac act gag gcc cag ccc tcc tgt gat agt gcc cct gcc ttg cag			2035
Gln Asp Thr Glu Ala Gln Pro Ser Cys Asp Ser Ala Pro Ala Leu Gln			
630	635	640	645

ccc ctg tta cac gca gtg aaa gct ggc agt ccc tca gag atg cca cgg		2083
Pro Leu Leu His Ala Val Lys Ala Gly Ser Pro Ser Glu Met Pro Arg		
650	655	660
gac tca ggc ata tat gat tct tct gta ccc tca tca gag ctc tct ctg		2131
Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu Ser Leu		
665	670	675
cct ctg atg gag gga ctc tcc ccg gat cag ata gaa aca tct tct ctg		2179
Pro Leu Met Glu Gly Leu Ser Pro Asp Gln Ile Glu Thr Ser Ser Leu		
680	685	690
acc gag agt gta tct tcc tcc tct ggc cta ggt gag gag gac ccc cct		2227
Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu Asp Pro Pro		
695	700	705
acc ctc cct tcc aag ctc ttt gcc tct ggg gtg tcc aga gaa cat ggt		2275
Thr Leu Pro Ser Lys Leu Phe Ala Ser Gly Val Ser Arg Glu His Gly		
710	715	720
tgc cac agc cac act gac gaa ctg caa gcg ctt gct cct ttg		2317
Cys His Ser His Thr Asp Glu Leu Gln Ala Leu Ala Pro Leu		
730	735	
taaggactcg gaagagtcta agcacgcgccttttagctgc tgatctctggctcccgat		2377
ttcacctctgtgtttgtca gcctacttgg agctgaaggc gcacacgggatatctggaa		2437
tgaat		2443
<210> 12		
<211> 739		
<212> PRT		
<213> Mouse		
<400> 12		
Met Ala Pro Trp Leu Gln Leu Cys Ser Phe Phe Phe Thr Val Asn Ala		
1	5	10
15		
Cys Leu Asn Gly Ser Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg		
20	25	30
30		
Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Gly Val Gly Pro Ala Ser		
35	40	45
45		
Arg Asn Ser Gly Leu His Asn Ile Thr Phe Arg Tyr Asp Asn Cys Thr		
50	55	60

Thr Tyr Leu Asn Pro Gly Gly Lys His Ala Ile Ala Asp Ala Gln
 65 70 75 80
 Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr
 85 90 95
 Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe
 100 105 110
 Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln
 115 120 125
 Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Arg Arg Thr
 130 135 140
 Gly Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr
 145 150 155 160
 Phe Val Lys Ile Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr
 165 170 175
 His Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Gln Pro
 180 185 190
 Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile
 195 200 205
 Ser Gln His Gly Ser Asp Met His Val Ser Phe Asp His Ala Pro Gln
 210 215 220
 Asn Phe Gly Phe Arg Gly Phe His Val Leu Tyr Lys Leu Lys His Glu
 225 230 235 240
 Gly Pro Phe Arg Arg Arg Thr Cys Arg Gln Asp Gln Asn Thr Glu Thr
 245 250 255
 Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu
 260 265 270
 Leu Val Asp Asp Ser Asn Thr Thr Arg Lys Ala Ala Gln Tyr Val Val
 275 280 285
 Lys Ser Val Gln Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile
 290 295 300
 Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val
 305 310 315 320
 Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu
 325 330 335
 Glu Ser Pro Glu Ser Ser Thr Tyr Ala Ala Ala Leu Pro Arg Asp Arg
 340 345 350
 Leu Arg Pro Gln Pro Lys Val Phe Leu Cys Tyr Ser Asn Lys Asp Gly
 355 360 365
 Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp
 370 375 380
 Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu
 385 390 395 400

Cys Arg Glu Gly Gln Arg Glu Trp Ala Ile Gln Lys Ile His Glu Ser
 405 410 415
 Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp
 420 425 430
 Lys Lys Asn Phe Arg His Lys Gly Gly Ser Arg Gly Glu Ala Gln Gly
 435 440 445
 Glu Phe Phe Leu Val Ala Val Ala Ala Ile Ala Glu Lys Leu Arg Gln
 450 455 460
 Ala Lys Gln Ser Ser Ala Ala Leu Arg Lys Phe Ile Ala Val Tyr
 465 470 475 480
 Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Cys Ser Leu Asp Leu Ser
 485 490 495
 Thr Lys Tyr Lys Leu Met Asp His Leu Pro Glu Leu Cys Ala His Leu
 500 505 510
 His Ser Gly Glu Gln Glu Val Leu Gly Gln His Pro Gly His Ser Ser
 515 520 525
 Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala
 530 535 540
 Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu
 545 550 555 560
 Lys Gln Phe Ile Pro Phe Gln His Pro Pro Val Arg Tyr Gln Glu Pro
 565 570 575
 Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Ile Ser
 580 585 590
 Lys Pro Gly Pro Glu Ser Asp Phe Cys Arg Lys Val Glu Ala Cys Val
 595 600 605
 Leu Gly Ala Ala Gly Pro Ala Asp Ser Tyr Ser Tyr Leu Glu Ser Gln
 610 615 620
 His Val Gly Leu Asp Gln Asp Thr Glu Ala Gln Pro Ser Cys Asp Ser
 625 630 635 640
 Ala Pro Ala Leu Gln Pro Leu Leu His Ala Val Lys Ala Gly Ser Pro
 645 650 655
 Ser Glu Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser
 660 665 670
 Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Pro Asp Gln Ile
 675 680 685
 Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly
 690 695 700
 Glu Glu Asp Pro Pro Thr Leu Pro Ser Lys Leu Phe Ala Ser Gly Val
 705 710 715 720
 Ser Arg Glu His Gly Cys His Ser His Thr Asp Glu Leu Gln Ala Leu
 725 730 735

Ala Pro Leu

<210> 13
 <211> 2217
 <212> DNA
 <213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the
 amino acid sequence of SEQ ID NO:12.

<221> misc_feature
 <222> (1)...(2217)
 <223> n = A, T, C or G

<400> 13

atggcncnt	ggytncaryt	ntgywsntt	ttyttyacng	tnaaygcntg	yytnaaaygg	60
wsncarytng	cngtngcngc	ngggngnwsn	ggnmgnngcnm	gngggngcnga	yacntgyggn	120
tggmngng	tnggncncg	nwsnmgnnaay	wsngngnytnc	ayaayathac	nttymgnhtay	180
gayaaytgya	cnaacntayt	naayccngn	ggngnaarc	aygcnathgc	ngaygcncar	240
aayathacna	thwsncarta	ygcntgycay	gaycargtng	cngtacnat	hytnrtggwsn	300
ccngngncny	tnggnathga	rtytynaar	ggnttymgn	tnathytna	rgarytnaar	360
wsngarggnm	gnccartgyc	rcarytnath	ytnaargayc	cnaacntayt	naaywsnwsn	420
ttymgnmgna	cnggnatgga	rwsncarccn	ttytynaaya	tgaarttgya	racngaytay	480
ttygtynaara	thgtncntt	yccnwsnath	aaraaygarw	snaaytayca	ycnnttym	540
ttymgnacnm	gngcngtgya	yytntyntn	carccngaya	ayytngcntg	yaarcnntt	600
tggarcnnm	gnaaytyna	yathwsncar	caygnwsng	ayatgcaygt	nwsnttym	660
caygcncnc	araaytgyg	nttymgnng	ttycaygtn	tntayaaryt	naarcaygar	720
ggncnttym	gnmgnmgnac	ntgymgnac	gaycaraaya	cngaracnac	nwsnttym	780
ytncaaraay	trwsncncng	ngaytayath	athgarytng	tngaygaw	naayacnacn	840
mgnnaargcng	cncartaygt	ngtnaawsn	gtncarwsnc	cntggcngg	nccnathmgn	900
gcnngtngcna	thacngtncc	nytngtngtn	athwsngcnt	tygcnacnyt	nttymgnht	960
atgtgymgn	araarcara	rgaraayath	taywsncayy	tngaygarga	rwsncncngar	1020
wsnwsnacnt	aygcngcngc	nytncnmgn	gaymgnym	gnccncarcc	naargtntt	1080
ytnntgytaw	snaayaarga	yggncaaraay	cayatgaayg	tngtncartg	yttymgnhtay	1140
ttytncarg	ayttytgygg	ntygargt	gcnytngay	tntgggarga	yttywsnyt	1200
tgymngarg	gnccarngn	rtggcncn	cararaathc	aygarwsnca	rttyathath	1260
gtngtntgyw	snaarggnat	gaarttayt	gtngayaara	araaytymg	ncayaarggn	1320
ggnwsnmng	ngngcnca	rggngartt	ttytngtng	cngtngcngc	nathgcngr	1380
aarytymgn	argcnacra	rwsnwsnwsn	gcnngn	gnarta	hgcngtn	1440
ttygatgtaw	sntgygargg	ngaytncn	tgywsnytng	ayytnwsnac	naartayaar	1500
ytnatggayc	ayytncn	rytntgygcn	cayytnca	sngngarca	rgargtnty	1560
gngncar	cayc	ws	nwsnmgmgn	aytayttym	gnwsnaarws	1620

ytntaygtng cnathtgyaa yatgcaycar ttyathgayg argarcnng aytggattygar aarcartya thccnttyca rcayccnccn gtnmgntayc argarcngt nytnagaraar ttygaywsng gnytnngtnt naaygaygtn athwsnaarc cnggnccnng rwsngaytay tgymgnaarg tngargcngt ygtnytnngn cngcngcngc cngcngayws ntaywsntay ytngarwsnc arcaygtngg nytngaycar gayacngarg cncarccnws ntgygaywsn gcncnccnngcny tncarcnnyt nytncaaygn gtnaargcng gnwsnccnws ngaratgccn mgngaywsng gnathayga ywsnwsgtn ccnwsnwsng arytnwsnyt nccnnytnatg garggnnytnw snccnngayca rathgaracn wswnwsnytna cngarwsngt nwsnwsnwsn wsnggnnytng gngargarga yccnccnacn ytnttgc nwsngngtng wsnmgngarc ayggntgyca ywsncayacn gaygartytnc argcnytngc nccnnytng	1680 1740 1800 1860 1920 1980 2040 2100 2160 2217
--	--